

GenCore version 5.1.3  
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OM protein - protein search, using sw modci

Run on: January 16, 2003, 16:40:32 ; Search time: 19:21:43 Seconds  
(without alignments)

56.562 Million cell updates/sec

Title: US-09-856-070-26

Perfect score 28

Sequence: QLYFF S

Scoring table: BLASTM52

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 20604715 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DR seq length: 0

Maximum DR seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTRIMBI\_21;\*

1: sp\_archaea;\*

2: sp\_bacteria;\*

3: sp\_lungi;\*

4: sp\_invertebrate;\*

5: sp\_human;\*

6: sp\_mammal;\*

7: sp\_mhc;\*

8: sp\_organelle;\*

9: sp\_phage;\*

10: sp\_plant;\*

11: sp\_protei;\*

12: sp\_virus;\*

13: sp\_vertebrate;\*

14: sp\_unclassified;\*

15: sp\_virus;\*

16: sp\_bacteriap;\*

17: sp\_archeap;\*

## ALIGNMENTS

### RESULT 1

ID	Q9H4N4	PRELIMINARY:	PRT;	106 AA.
AC	Q9H4N4			
DT	01-MAR-2001 (TREMBL); 16, created			
DT	01-MAR-2001 (TREMBL); 16, last sequence update			
DT	01-MAR-2001 (TREMBL); 16, last annotation update			
DE	Clone CDAB0082 mRNA sequence.			
OS	Homo sapiens (Human)			
OC	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
OX	NCBI_TAXID:9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-97267237; PubMed-9110174;			
RA	Yu W., Andersson B., Worley K.C., Muzny D.M., Ding Y., Liu W.,			
RA	Anderson R., Wentland M.A., Ricafrente J.Y., Liu W., Gibbs R.A.; Large scale cDNA sequencing;			
PT	"A" double adapter method for improved shotgun library construction."			
PT	Anal. Biochem. 236:107-113(1996).			
RL	[2]			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE-97267237; PubMed-9110174;			
RA	Yu W., Andersson B., Worley K.C., Muzny D.M., Ding Y., Liu W.,			
RA	Anderson R., Wentland M.A., Ricafrente J.Y., Liu W., Gibbs R.A.; Large scale cDNA sequencing;			
RA	"A" double adapter method for improved shotgun library construction."			
PT	Anal. Biochem. 236:107-113(1996).			
RL	[2]			

Q9H4N4 home sapien  
Q9KE60 bacterius ha

Q9P74 haemarchia

Q91706 streptococcus

Q92392 xenopus lae

Q97344 streptomyces

Q9P117 xestia cini

Q93497 caenorhabditis

Q9V1K3 drosophila

Q8U0I3 rattus norvegicus

Q9JIK3 volvox carteri

Q24542

Q9WZQ3 thermotoga

Q9WZG3

Q9WZQ3

RESULT No.	Score	Match length	DB	ID	Description
1	28	100.0	106	4	Q9H4N4
2	28	100.0	125	5	Q9F217
3	28	100.0	130	16	Q9K660
4	28	100.0	156	16	Q9KU11
5	28	100.0	171	2	Q50138
6	28	100.0	179	5	Q9P74
7	28	100.0	263	16	Q97NV2
8	28	100.0	260	1	Q9F700
9	28	100.0	315	13	Q03292
10	28	100.0	361	16	Q97SA4
11	28	100.0	370	12	Q9P217
12	28	100.0	376	5	Q96GW7
13	28	100.0	400	5	Q9V1K3
14	28	100.0	404	5	Q9T0T3
15	28	100.0	406	11	Q9JIK3
16	28	100.0	444	19	Q24542

## SUMMARIES

### 8

RESULT No.	Score	Match length	DB	ID	Description
1	28	100.0	106	4	Q9H4N4
2	28	100.0	125	5	Q9F217
3	28	100.0	130	16	Q9K660
4	28	100.0	156	16	Q9KU11
5	28	100.0	171	2	Q50138
6	28	100.0	179	5	Q9P74
7	28	100.0	263	16	Q97NV2
8	28	100.0	260	1	Q9F700
9	28	100.0	315	13	Q03292
10	28	100.0	361	16	Q97SA4
11	28	100.0	370	12	Q9P217
12	28	100.0	376	5	Q96GW7
13	28	100.0	400	5	Q9V1K3
14	28	100.0	404	5	Q9T0T3
15	28	100.0	406	11	Q9JIK3
16	28	100.0	444	19	Q24542

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

## 8

RESULT No.	Score	Match length	DB	ID	Description
1	28	100.0	106	4	Q9H4N4
2	28	100.0	125	5	Q9F217
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12	28	100.0	376	5	Q96GW7
13	28	100.0	400	5	Q9V1K3
14	28	100.0	404	5	Q9T0T3
15	28	100.0	406	11	Q9JIK3
16	28	100.0	444	19	Q24542

Best Local Similarity 100.0%; Score 28; DR 4; Length 106; Matches 5; conservative 0%; Mismatches 0%; Indels 0%; Gaps 0%;

Query 1 GOSEE 5

Db	53 QDYEE 57	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	QY 1 QDYEE 5 1111 Db 81 QDYEE 85
<b>RESULT 2</b>			
1D	G45212 PRELIMINARY;	PRT; 125 AA.	
AC	045212;		
DT	01-JUN-1998 (TREMBL), 06, Created		
DT	01-JUN-1998 (TREMBL), 06, Last sequence update		
DE	Tropomin (Fragment)		
OS	Baculia pallidii		
OC	Onchocercidae; Brugidae		
OX	NCHI_TaxID-6280;		
KN	11		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-SUS;		
RI	Hunter S.J.;		
RI	submitted (MAR 1998) to the EMBL/GenBank/DDBJ databases		
KN	121		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-SUS;		
RX	MEDLINE-97001686; PubMed-8844678;		
RA	Martin S.A.M., Hunter S.J., Thompson F.J., Devaney E.,		
RA	"Strange specific gene expression in the post-infective t.3 of the filarial nematode, Brugia pahangi,"		
RL	Sci. Biol. Biochem. Parasitol. 79:109-112(1996).		
DR	AJ224967; CAA12266; 1;		
FT	125		
SQ	SEQUENCE 125 AA: 1454 MW, ZFAIRFKAQKQFEECFPFC4,		
Query Match	100.0%	Score 28; DB 5; Length 25;	
Best Local Similarity	100.0%	Pred. No. 72;	
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0; C;			
QY 1 QDYEE 5 1111 Db 89 QDYEE 93			
<b>RESULT 3</b>			
1D	Q9K660 PRELIMINARY;	PRT; 130 AA.	
AC	Q9K660;		
DT	01-OCT-2000 (TREMBL), 15, Created		
DT	01-OCT-2000 (TREMBL), 15, Last sequence update		
DE	Hypothetical protein BH3872.		
GR	BB4B2.		
OS	Bacillus halodurans		
OC	Bacteria; Firmicutes; Bacillus/Clostridium group, Bacillidiace,		
OC	Bacillaceae; Bacillus		
OX	NCBI_TaxID-86665;		
KN	111		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-SUS;		
RX	MEDLINE-2051582; PubMed-11058132;		
RA	Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N., Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S., Horikoshi K.		
RA	"Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic comparison with <i>Bacillus subtilis</i> ."		
RL	Nucleic Acids Res. 28:4317-4331(2000).		
DR	EMBL: AB001511; DAB05127; 1;		
DR	InterPro: IPR00122; SGN5; acetyltransfer.		
DR	pfam: PF00583; Acetyltransfer_1.		
KW	Hypothetical protein; Complete proteome.		
SQ	SEQUENCE 156 AA: 17825 MW; 87GE0FE1551F612D CRC64;		
Query Match	100.0%	Score 28; DB 16; Length 156;	
Best Local Similarity	100.0%	Pred. No. 93;	
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY 1 QDYEE 5 1111 Db 9 QDYEE 13			
<b>RESULT 4</b>			
1D	Q9K660 PRELIMINARY;	PRT; 130 AA.	
AC	Q9K660;		
DT	01-OCT-2000 (TREMBL), 15, Created		
DT	01-OCT-2000 (TREMBL), 15, Last sequence update		
DE	Hypothetical protein BH3872.		
GR	BB4B2.		
OS	Bacillus halodurans		
OC	Bacteria; Firmicutes; Bacillus/Clostridium group, Clostridiace;		
OC	Clostridiiales; Lachnospiraceae; Ruminococcus.		
OX	NCBI_TaxID-1264;		
RN	111		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-SUS;		
RA	Umemori J., Miwa T., Nagamine T., Ogata K., Takenaka A., Hino T., Horikoshi K.		
RA	"Sequence analysis of the gene coding proton-translocating ATPase of <i>Ruminococcus albus</i> ."		
RT	Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.		
RI	DR: AB006151; BAA23684; 1;		
DR	InterPro: IPR002146; ATPSynt_B/B' sub.		
DR	Pfam: PF00430; ATP_Synth_B;		
DR	TIGRFAMS: TIGR0144; ATP_Synth_b;		
SQ	SEQUENCE 171 AA: 19247 MW; 464KE7417472F120 CRC64;		
Query Match	100.0%	Score 28; DB 2; Length 171;	
Best Local Similarity	100.0%	Pred. No. 75;	



DR	HSSP; P27986; LPHT;	RP	RN [1]
DR	InterPro; IPR01452; SH3.	RP	SEQUENCE FROM N.A.
DR	Protein; PF00018; SH3.	RX	RP MEDLINE: 9943230; PubMed: 10502508;
DR	PRINTS; PR00452; SH3OMA_N.	RA	RA Hayakawa T., Ko R., Okano K., Seong S.J., Goto C., Maeda S.;
DR	SMART; SM00066; SH3_1.	RT	RT *Sequence analysis of the Xestia c-nigrum granulovirus genome.*;
DR	SMASH; SM0026; SH3_1.	PL	PL VIBI-047 262 277-297(1999)
DR	PROSITE; PS50002; SH3_1.	DR	DR EMBL: AF162221; AACF05140.1; -
KW	SEQUENCE domain.	SQ	SQ SEQUENCE 370 AA; 4.2913 MW; 4EFDAA45F05CCB4 CRC64;
SO	SEQUENCE 315 AA; 34257 MW; A517FE20AA017AF CRC64;	Query	Query Match 100.0%; Score 28; DB 12; Length 370;
		Best Local Similarity 100.0%; Pred. No. 2; e-02;	Best Local Similarity 100.0%; Pred. No. 2; e-02;
	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 QDYE 5	QY	1 QDYE 5
DB	226 QWYEE 230	DB	151 QDYE 155
RESULT 10	Q97RA4 PRELIMINARY; PR: 361 AA.	RESULT 12	Q95QW7 PRELIMINARY; PR: 376 AA.
ID	Q97RA4; PR: 361 AA.	ID	Q95QW7; PR: 376 AA.
AC	Q97RA4; PR: 361 AA.	AC	Q95QW7; PR: 376 AA.
DT	01-OCT-2001 (TREMBLrel. 18, Created)	DT	01-OCT-2001 (TREMBLrel. 19, Created)
DT	01-OCT-2001 (TREMBLrel. 18, Last sequence update)	DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)	DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE	Hypothetical protein SP0921.	DE	Hypothetical 44.4 kDa protein.
GN	SP0921.	GN	C1475.3.
GS	Streptococcus pneumoniae	OS	Caenorhabditis elegans.
OC	Bacteria; Firmicutes; Clostridium group, Lactobacillales;	OC	Eukaryota; Metazoa; Nematoda; Chordata; Rhabditoidea;
OC	Streptococcaceae; Streptococcus.	OC	Rhabditida; Pseudorhabditida; Caenorhabditis;
OX	NCBI_TaxID-1313;	OX	NCBI_TaxID-6239;
RN	SEQUENCE FROM N.A.	RN	[1]
RP	STRAIN-BRISTOL_N2;	RP	SEQUENCE FROM N.A.
RC	MEDLINE: 99066613; PubMed: 9851916;	RC	RP
RA	None;	RA	RA
PT	*Genome sequence of the nematode <i>C. elegans</i> , a platform for investigating biology. The <i>C. elegans</i> Sequencing Consortium. Science 282:401-410 (1998).	PT	PT
RL		RL	RL
RN		RN	RN [2]
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
RC	STRAIN-BRISTOL_N2;	RC	RC
RA	Waterson R.;	RA	RA
PT	"Direct Submission."	PT	PT
RT	Submitted (Com-2001) to the EMBL/GenBank/DDBJ databases.	RT	RT
RI	Submitted (Jun-1995) to the EMBL/GenBank/DDBJ databases.	RI	RI
RN	[3]	RN	RN [3]
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
RC	STRAIN-BRISTOL_N2;	RC	RC
RA	Waterson R.;	RA	RA
PT	"Direct Submission."	PT	PT
RT	Submitted (Com-2001) to the EMBL/GenBank/DDBJ databases.	RT	RT
RI	Submitted (Jun-1995) to the EMBL/GenBank/DDBJ databases.	RI	RI
RN		RN	RN [3]
RP		RP	RP
RC		RC	RC
RA		RA	RA
PT		PT	PT
RT		RT	RT
RI		RI	RI
QY	1 QDYE 5	QY	1 QDYE 5
DB	124 QWYEE 127	DB	99 QDYE 103
RESULT 11	Q9PZ7 PRELIMINARY; PR: 370 AA.	RESULT 13	Q9VFC9 PRELIMINARY; PR: 400 AA.
ID	Q9PZ7; PR: 370 AA.	ID	Q9VFC9; PR: 400 AA.
AC	Q9PZ7; PR: 370 AA.	AC	Q9VFC9;
DT	01-MAY-2000 (TREMBLrel. 13, Created)	DT	01-MAY-2000 (TREMBLrel. 13, Created)
DT	01-DEC-2001 (TREMBLrel. 13, Last sequence update)	DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT	01-DEC-2001 (TREMBLrel. 13, Last annotation update)	DT	01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE	Xestia c-nigrum granulosis virus (XCV) (Xestia c-nigrum granulovirus).	DE	XCV protein.
GS	Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Granulovirus	GS	CG1987 protein.
OC		OC	CG1987.
OX	NCBI_TaxID-51677;	OX	NCBI_TaxID-51677;

OS	Drosophila melanogaster (Fruit fly).	OX	NCBI_TAXID=7227;
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta,	RN	[1]
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha,	RP	SEQUENCE FROM N.A.
OC	Dipteroidea; Drosophilidae; Drosophila.	RC	STRAIN=BERKELEY,
ON		RA	Stapleton M., Brokstein P., Dorsett V., Farfan D., Frise E., George P.,
PN		PA	Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George P.,
PP	SEQUENCE FROM N.A.	PA	Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mongalli C.,
PX		PA	Nunoo J., Parikh J., Parajag V., Park S., Phuanoung S., Wan K.,
MENDEL_NID=20196306; PubMed=10731132;		PA	Yiu C., Lewis S.E., Rubin G.M., Celinkiner S.
RA	Adams M.D., Celinkiner S.E., Holt R.A., Evans C.A., Gocayne J.D.,	PI	Submitted (MENDEL_NID) to the EMBL/Sonnenburg/DDBJ databases
RA	Amanatides P.G., Scherer S.E., li P.W., Ashburner M., Henderson S.N.,	DR	AY006974; AALL9219.1; -.
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,	SQ	SEQUENCE 4nd4 AA: 4Ku6i MW;
RA	Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,		2E305852FEE93158 CRC64;
RA	Brandao R.C., Rogers Y.-H.C., Blaize C., Champe M., Pfeiffer B.D.,		
RA	Wang K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,		
RA	Abril J.F., Aboyanian A., Au H.-J., Andriesse-Painkovich C., Baldwin B.,		
RA	Baldwin R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,		
RA	Berman B.P., Bhandari D., Bolshakov S.,		
RA	Borkova D., Boilash M.R., Bouck J., Broksius P., Brottier P.,		
RA	Burtsis K.C., Busam D.A., Buttler H., Cadieu F., Center A., Chandra I.,		
RA	Cherry J.M., Cawley S., Dahake C., Davenport L.B., Davies P.,		
RA	de Pablo B., Delcher A., Deng Z., Mays A.B., Dew I., Dietz S.M.,		
RA	Deudon K., Dicup L.F., Edwards M., Ferguson S., Fonkoue H.C., Dunn P.,		
RA	Durbin R.T., Evangelista R.C., Ferreria S., Fleischmann W.,	RESULT 15	
RA	Foster C., Gabrielista R.C., Ferreria S., Fleischmann W.,	Q9JIK3	
RA	Foster C., Gabrielista R.C., Ferreria S., Fleischmann W.,	TD	SEQUENCE FROM N.A.
RA	Gidekel A., Goog F., Gourieau T.H., Guo Z., Guilan P., Glasser K.,	Q9JIK3	
RA	Harris N.L., Harvey D., Heiman L.J., Hernández I.R., Hurk J.,	AA	
RA	Houston D., Houston K.A., Howland P.T., wei M.-H., Ibergawm C.,	Q9JIK3	
RA	Jalali M., Kalush F., Karpen G.H., Ko Z., Kennison J.A., Ketchem K.A.,	Q9JIK3	
RA	Kimmel R.E., Kodira C., Kraft C., Kravitz S., Kulp D., Lai Z.,	Q9JIK3	
RA	Lasko P., Lai Y., Levitt A.A., Li J., Li Z., Liang Y., Lin X.,	Q9JIK3	
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,	Q9JIK3	
RA	Menkulov G., Milashina N.V., Mobarry C., Morris J., Moskrafi A.,	Q9JIK3	
RA	Mount M., Moy M., Murphy R., Murphy D.M., Nelson D.J.,	Q9JIK3	
RA	Nelson D.M., Nelson K.A., Nixon K., Nussken D.B., Pacifici J.M.,	Q9JIK3	
RA	Paluszak M., Pittman C.S., Pan S., Pollard J., Puij V., Reese M.G.,	Q9JIK3	
RA	Reinert K., Remington K., Saunders R.D.C., Scheerer F., Shen H.,	Q9JIK3	
RA	Shue B.C., Siden-Kiamos I., Simpson M., Strong P., Sun F., Smith T.,	Q9JIK3	
RA	Spier F., Spradling A.C., Stapleton M., Strong P., Sun F., Smith T.,	Q9JIK3	
RA	Svirskas R., Trotter C., Turner R., Veltman K., Wang A., Wang X.,	Q9JIK3	
RA	Wang Y.-Y., Wasserman I.A., Weinstock G.M., Weissbecker J.,	Q9JIK3	
RA	Williams S.M., Woodage T., Wooley K.C., Wu D., Yang S., Yao Q.A.,	Q9JIK3	
RA	Ye J., Yeh R.-F., Zaveri J.S., Zhao M., Zhou X., Zhu S., Zhu X.,	Q9JIK3	
RA	Zheng X.H., Zheng F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,	Q9JIK3	
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venetor A.,	Q9JIK3	
RT	Science 287:2187-2195 (2000);	Q9JIK3	
F	EMBL AE006717; AAC53411.	Q9JIK3	
DR	Pfizerbase; FBgn0038292; CG33087;	Q9JIK3	
SQ	SEQUENCE 4.00 AA: 4K6334 MW;	Q9JIK3	
Query Match 100.0%; Score 28; DB 5; Length 400;			Score 28; DB 5; Length 400;
Best local Similarity 100.0%; Pred. No. 2.7e-02;			Best local Similarity 100.0%; Pred. No. 2.7e-02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 QDYE 5	QY	1 QDYE 5
DB	44 QDYE 48	DB	353 QDYE 357
			Search completed, January 16, 2003, 16:55:49
			Job time : 20:21:43 secs

